



SEQUENCE LISTING

<110> Haruo HANAWA

<120> VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING TARGET  
PROTEIN IN MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION  
OF THE VECTOR FOR GENE THERAPY

<130> 0760-0347PUS1

<140> US 10/541,626

<141> 2005-07-07

<150> PCT/JP2003/016956

<151> 2003-12-26

<150> JP 2003-3967

<151> 2003-01-10

<160> 24

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> oligopeptide C19-29 region of glucagon of human, mouse or rat

<400> 1

Ala	Gln	Asp	Phe	Val	Gln	Trp	Leu	Met	Asn	Thr
1				5					10	

<210> 2

<211> 1471

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region  
and glucagon C19-29 region

<220>

<221> CDS

<222> (13)..(1461)

<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region  
and glucagon C19-29 region

<400> 2

gaattcattt	aa	atg	att	ctg	ctg	gtg	gtc	ctg	atg	ctg	tct	gcg	gag	atc	51
		Met	Ile	Leu	Leu	Val	Val	Leu	Met	Leu	Ser	Ala	Glu	Ile	
		1				5						10			

ggg	agt	gga	gct	ttg	atg	agc	acc	gag	gat	cct	aag	ccg	ccc	tcg	gtg	99
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Gly	Ser	Gly	Ala	Leu	Met	Ser	Thr	Glu	Asp	Pro	Lys	Pro	Pro	Ser	Val	
15						20					25					
cct	gcg	cca	aca	aat	gtt	cta	att	acg	tcc	tat	gac	ttg	aac	cct	gtc	147
Pro	Ala	Pro	Thr	Asn	Val	Leu	Ile	Thr	Ser	Tyr	Asp	Leu	Asn	Pro	Val	
30					35					40					45	
gta	cat	tgg	aag	cac	cag	aac	gtg	tcg	cag	gct	gcc	gtc	ttc	act	gta	195
Val	His	Trp	Lys	His	Gln	Asn	Val	Ser	Gln	Ala	Ala	Val	Phe	Thr	Val	
				50					55					60		
cag	gta	aag	atg	tat	cca	gaa	tac	tgg	act	gat	gcc	tgc	acc	aac	att	243
Gln	Val	Lys	Met	Tyr	Pro	Glu	Tyr	Trp	Thr	Asp	Ala	Cys	Thr	Asn	Ile	
			65					70					75			
gcc	cat	cat	tat	tgt	aat	atc	tac	aaa	cac	att	tcc	tat	cct	gac	tca	291
Ala	His	His	Tyr	Cys	Asn	Ile	Tyr	Lys	His	Ile	Ser	Tyr	Pro	Asp	Ser	
		80					85					90				
tct	gcc	tgg	gcc	aga	gtt	aag	gcc	aag	gtt	gga	caa	aga	gaa	tct	gcc	339
Ser	Ala	Trp	Ala	Arg	Val	Lys	Ala	Lys	Val	Gly	Gln	Arg	Glu	Ser	Ala	
	95					100					105					
tat	gcg	cag	tca	gaa	gag	ttt	att	atg	tgc	cga	aag	ggg	aag	gtt	gga	387
Tyr	Ala	Gln	Ser	Glu	Glu	Phe	Ile	Met	Cys	Arg	Lys	Gly	Lys	Val	Gly	
110					115				120						125	
ccg	cct	ggc	ctg	gac	atc	gga	agg	aag	gaa	gat	cag	ctg	att	gtc	cac	435
Pro	Pro	Gly	Leu	Asp	Ile	Gly	Arg	Lys	Glu	Asp	Gln	Leu	Ile	Val	His	
				130					135					140		
ata	ttt	cac	cct	aag	gtc	aat	gtg	agt	cag	gaa	acc	atg	ttt	ggt	gac	483
Ile	Phe	His	Pro	Lys	Val	Asn	Val	Ser	Gln	Glu	Thr	Met	Phe	Gly	Asp	
			145					150					155			
gga	aat	acc	tgt	tac	aca	ttc	gac	tac	act	gtg	ttt	gtg	aaa	cat	tac	531
Gly	Asn	Thr	Cys	Tyr	Thr	Phe	Asp	Tyr	Thr	Val	Phe	Val	Lys	His	Tyr	
		160					165					170				
agg	agt	ggg	gag	atc	cta	cat	aca	gaa	cat	agc	gtc	cta	aaa	gaa	gat	579
Arg	Ser	Gly	Glu	Ile	Leu	His	Thr	Glu	His	Ser	Val	Leu	Lys	Glu	Asp	
	175					180					185					
tgt	agc	gaa	act	ctg	tgt	gag	tta	aac	atc	tca	gtg	tcc	acg	ctg	aat	627
Cys	Ser	Glu	Thr	Leu	Cys	Glu	Leu	Asn	Ile	Ser	Val	Ser	Thr	Leu	Asn	
190					195					200					205	
tcc	aat	tac	tgt	gtt	tca	gta	gtt	gga	aag	tcg	tct	ttc	tgg	caa	gtt	675
Ser	Asn	Tyr	Cys	Val	Ser	Val	Val	Gly	Lys	Ser	Ser	Phe	Trp	Gln	Val	
				210					215					220		
aat	aca	gaa	aca	tca	aaa	gac	gcc	tgt	atc	ccc	ttt	ctc	cat	gat	gac	723
Asn	Thr	Glu	Thr	Ser	Lys	Asp	Ala	Cys	Ile	Pro	Phe	Leu	His	Asp	Asp	
			225					230					235			
aga	gaa	gaa	gcg	gcc	gcc	gtg	ccc	aga	aac	tgt	gga	ggt	gat	tgc	aag	771
Arg	Glu	Glu	Ala	Ala	Ala	Val	Pro	Arg	Asn	Cys	Gly	Gly	Asp	Cys	Lys	

240	245	250	
cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro 255 260 265			819
cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr 270 275 280 285			867
tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser 290 295 300			915
tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro 305 310 315			963
gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile 320 325 330			1011
ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr 335 340 345			1059
agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu 350 355 360 365			1107
ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu 370 375 380			1155
gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe 385 390 395			1203
tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln 400 405 410			1251
gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr 415 420 425			1299
ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly 430 435 440 445			1347
aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His 450 455 460			1395
act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val 465 470 475			1443

cag tgg ttg atg aat acc tgagaattct  
 Gln Trp Leu Met Asn Thr  
 480

1471

<210> 3  
 <211> 4790  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA sequence of artificial expression vector pCAGGS

<400> 3  
 gtcgacattg attattgact agttattaat agtaatcaat tacgggggtca ttagttcata 60  
 gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgctt ggctgaccgc 120  
 ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180  
 ggactttcca ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac 240  
 atcaagtgtg tcatatgcca agtacgcccc ctattgacgt caatgacggg aaatggcccc 300  
 cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360  
 tattagtcat cgctattacc atgggtcgag gtgagcccca cgttctgctt cactctcccc 420  
 atctcccccc cctccccacc cccaattttg tatttattta ttttttaatt attttgtgca 480  
 gcgatggggg cggggggggg gggggcgcg gccaggcggg gcggggcggg gcgagggggc 540  
 gggcgggggc aggcggagag gtgcggcggc agccaatcag agcggcgcgc tccgaaagtt 600  
 tccttttatg gcgagggcg gcggcgggcg gccctataaa aagcgaagcg cgcgggcggc 660  
 gggagtcgct gcgttgctt cgccccgtgc cccgctccgc gccgcctcgc gccgcccgcc 720  
 ccggctctga ctgaccgct tactcccaca ggtgagcggg cgggacggcc cttctcctcc 780  
 gggctgtaat tagcgcttgg tttaatgacg gctcgtttct tttctgtggc tgcgtgaaag 840  
 ccttaaaggg ctccgggagg gccctttgtg cgggggggag cggctcgggg ggtgcgtgcg 900  
 tgtgtgtgtg cgtggggagc gccgcgtgcg gcccgcgctg cccggcggtt gtgagcgctg 960  
 cgggcgcggc gcggggcttt gtgcgctccg cgtgtgcgcg aggggagcgc ggccgggggc 1020  
 ggtgccccgc ggtgcggggg ggctgcgagg ggaacaaagg ctgcgtgcgg ggtgtgtgcg 1080  
 tgggggggtg agcagggggg gtgggcgcgg cggtcgggct gtaaccccc cctgcacccc 1140  
 cctccccgag ttgctgagca cggcccggct tcgggtgcgg ggctccgtgc ggggcgtggc 1200  
 gcggggctcg ccgtgccggg cgggggggtg cggcaggtg gggtgccggg cggggcgggg 1260

ccgcctcggg	ccggggaggg	ctcgggggag	gggcgcggcg	gccccggagc	gccggcggct	1320
gtcgaggcgc	ggcgagccgc	agccattgcc	ttttatggta	atcgtgcgag	agggcgcagg	1380
gacttccttt	gtcccaaate	tggcggagcc	gaaatctggg	aggcgccgcc	gcacccccctc	1440
tagcgggcgc	gggcgaagcg	gtgcggcgcc	ggcaggaagg	aaatgggcgg	ggagggcctt	1500
cgtgcgtcgc	cgcgcgcgcg	tcccccttctc	catctccagc	ctcggggctg	ccgcaggggg	1560
acggctgcct	tcggggggga	cggggcaggg	cgggggttcgg	cttctggcgt	gtgaccggcg	1620
gctctagagc	ctctgctaac	catgttcattg	ccttcttctt	tttctacag	ctcctgggca	1680
acgtgctggt	tgttgctgtg	tctcatcatt	ttggcaaaga	attcctcgag	gaattcactc	1740
ctcaggtgca	ggctgcctat	cagaagggtg	tggctggtgt	ggccaatgcc	ctggctcaca	1800
aataccactg	agatcttttt	ccctctgcc	aaaattatgg	ggacatcatg	aagccccttg	1860
agcatctgac	ttctggctaa	taaaggaaat	ttattttcat	tgcaatagt	tgttggaatt	1920
ttttgtgtct	ctcactcgga	aggacatatg	ggagggcaaa	tcatttaaaa	catcagaatg	1980
agtatttggt	ttagagtttg	gcaacatatg	ccatatgctg	gctgccatga	acaaagggtg	2040
ctataaagag	gtcatcagta	tatgaaacag	ccccctgctg	tccattcctt	attccataga	2100
aaagccttga	cttgagggtta	gatttttttt	atattttggt	ttgtgttatt	tttttcttta	2160
acatccctaa	aattttcctt	acatgtttta	ctagccagat	ttttcctcct	ctcctgacta	2220
ctcccagtca	tagctgtccc	tcttctctta	tgaagatccc	tcgacctgca	gccaagctt	2280
ggcgtaatca	tggctatagc	tgtttctctg	gtgaaattgt	tatccgctca	caattccaca	2340
caacatacga	gccggaagca	taaagtgtaa	agcctggggt	gcctaatgag	tgagctaact	2400
cacattaatt	gcgttgcgct	cactgcccgc	tttccagtcg	ggaaacctgt	cgtgccagcg	2460
gatccgcctc	tcaattagtc	agcaaccata	gtcccgcccc	taactccgcc	catcccgccc	2520
ctaactccgc	ccagttccgc	ccatttctccg	ccccatggct	gactaatttt	ttttatttat	2580
gcagaggccg	aggccgcctc	ggcctctgag	ctattccaga	agtagtgagg	aggctttttt	2640
ggaggccctag	gcttttgcaa	aaagctaact	tgtttattgc	agcttataat	ggttacaaat	2700
aaagcaatag	catcacaaat	ttcacaaata	aagcattttt	ttcactgcat	tctagttgtg	2760
gtttgtccaa	actcatcaat	gtatcttata	atgtctggat	ccgctgcatt	aatgaatcgg	2820
ccaacgcgcg	gggagaggcg	gtttgcgtat	tgggcgctct	tccgcttcct	cgctcactga	2880
ctcgctgcgc	tcggtcgttc	ggctgcggcg	agcggtatca	gctcactcaa	aggcggtaat	2940
acggttatcc	acagaatcag	gggataacgc	aggaaagaac	atgtgagcaa	aaggccagca	3000

aaaggccagg aaccgtaaaa aggccgcggtt gctggcggttt ttccataggc tccgcccccc	3060
tgacgagcat cacaaaaatc gacgctcaag tcagagggtg cgaaacccga caggactata	3120
aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc	3180
gcttaccgga tacctgtccg cttttctccc ttcggaagc gtggcgcttt ctcaatgctc	3240
acgctgtagg tatctcagtt cgggtgtaggt cgttcgctcc aagctgggct gtgtgcacga	3300
acccccggtt cagcccgaac gctgcgcctt atccggtaac tatcgtcttg agtccaaccc	3360
ggtaagacac gacttatcgc cactggcagc agccactggg aacaggatta gcagagcgag	3420
gtatgtaggc ggtgctacag agttcttgaa gtgggtggcct aactacggct aactagaag	3480
gacagtatth ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag	3540
ctcttgatcc ggcaaacaaa ccaccgctgg tagcgggtgg ttttttgttt gcaagcagca	3600
gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga	3660
cgctcagtg aacgaaaaact cacgttaagg gattttggtc atgagattat caaaaaggat	3720
cttcacctag atcctttttaa attaaaaatg aagttttaaa tcaatctaaa gtatatatga	3780
gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct cagcgatctg	3840
tctatttcgt tcatccatag ttgcctgact ccccgctcgt tagataacta cgatacggga	3900
gggcttacca tctggcccca gtgctgcaat gataccgcga gaccacgct caccggctcc	3960
agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg gtcctgcaac	4020
tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa gtagttcgcc	4080
agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cacgctcgtc	4140
gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta catgatcccc	4200
catgttggtc aaaaaagcgg ttagctcctt cggtcctccg atcgttggtc gaagtaagtt	4260
ggcgcagtg ttatcactca tggttatggc agcactgcat aattctctta ctgtcatgcc	4320
atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct gagaatagt	4380
tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg cgccacatag	4440
cagaacttta aaagtgtca tcattggaaa acgttcttcg gggcgaaaac tctcaaggat	4500
cttaccgtg ttgagatcca gttcgatgta acccactcgt gcacccaact gatcttcagc	4560
atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa	4620
aaaggaata agggcgacac ggaaatgttg aatactcata ctcttccttt ttcaatatta	4680

ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat gtatttagaa 4740  
aaataaaca ataggggttc cgcgcacatt tccccgaaaa gtgccacctg 4790

<210> 4  
<211> 1233  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA insert encoding rat CTLA4, rat IgG Fc region and glucagon C19-29 region

<220>  
<221> CDS  
<222> (13)..(1224)  
<223> DNA insert encoding rat CTLA4, rat IgG Fc region and glucagon C19-29 region

<400> 4  
gaattcattt aa atg gct tgt ctt gga ctc cag agg tac aaa act cac ctg 51  
Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu  
1 5 10  
cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc 99  
Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu  
15 20 25  
ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg 147  
Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val  
30 35 40 45  
gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat gca 195  
Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala  
50 55 60  
tct tca cac aac act gat gag gtc cgg gtg acg gtg ctg cgg cag aca 243  
Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr  
65 70 75  
aat gac caa gtg aca gag gtc tgt gcc acg aca ttc aca gtg aag aac 291  
Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn  
80 85 90  
acg ttg ggc ttc cta gat gac ccc ttc tgc agt ggt acc ttt aat gaa 339  
Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu  
95 100 105  
agc aga gtg aac ctc acc atc caa gga ctg agg gct gct gac acc gga 387  
Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly  
110 115 120 125  
ctg tac ttc tgc aag gtg gaa ctc atg tac cca ccg cca tac ttt gtg 435  
Leu Tyr Phe Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val  
130 135 140

ggc atg ggc aac ggg acc cag att tat gtc atc gat cca gaa cca tgc Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys 145 150 155	483
cca gat tca gac gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc Pro Asp Ser Asp Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys 160 165 170	531
aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe 175 180 185	579
ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val 190 195 200 205	627
acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe 210 215 220	675
agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro 225 230 235	723
cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro 240 245 250	771
atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val 255 260 265	819
acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro 270 275 280 285	867
gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys 290 295 300	915
gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly 305 310 315	963
ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro 320 325 330	1011
cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser 335 340 345	1059
tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln 350 355 360 365	1107
gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac	1155



Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His	
370 375 380	
cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt	1203
His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe	
385 390 395	
gtg cag tgg ttg atg aat acc tgagaattc	1233
Val Gln Trp Leu Met Asn Thr	
400	
<210> 5	
<211> 1143	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> DNA insert encoding rat IL13, rat IgG Fc region and glucagon C19-29 region	
<220>	
<221> CDS	
<222> (13)..(1134)	
<223> DNA insert encoding rat IL13, rat IgG Fc region and glucagon C19-29 region	
<400> 5	
gaattcatTTT aa atg gca ctc tgg gtg act gca gtc ctg gct ctc gct tgc	51
Met Ala Leu Trp Val Thr Ala Val Leu Ala Leu Ala Cys	
1 5 10	
ctt ggt ggt ctt gcc acc cca ggg cca gtg cgg aga tcc aca tct ccc	99
Leu Gly Gly Leu Ala Thr Pro Gly Pro Val Arg Arg Ser Thr Ser Pro	
15 20 25	
cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa	147
Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln	
30 35 40 45	
gac cag aag act tcc ctg tgc aac agc agc atg gta tgg agc gtg gac	195
Asp Gln Lys Thr Ser Leu Cys Asn Ser Ser Met Val Trp Ser Val Asp	
50 55 60	
ctg aca gct ggc ggg ttc tgt gca gcc ctg gaa tcc ctg acc aac atc	243
Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile	
65 70 75	
tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc	291
Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu	
80 85 90	
tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa	339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys	
95 100 105	
atc gaa gta gcc cag ttt ata tca aaa ctg ctc aat tac tcc aag caa	387

Ile	Glu	Val	Ala	Gln	Phe	Ile	Ser	Lys	Leu	Leu	Asn	Tyr	Ser	Lys	Gln		
110					115					120					125		
ctt	ttc	cgc	tat	ggc	cac	gcg	gcc	gcc	gtg	ccc	aga	aac	tgt	gga	ggg	435	
Leu	Phe	Arg	Tyr	Gly	His	Ala	Ala	Ala	Val	Pro	Arg	Asn	Cys	Gly	Gly		
				130					135					140			
gat	tgc	aag	cct	tgt	ata	tgt	aca	ggc	tca	gaa	gta	tca	tct	gtc	ttc	483	
Asp	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Gly	Ser	Glu	Val	Ser	Ser	Val	Phe		
			145					150					155				
atc	ttc	ccc	cca	aag	ccc	aaa	gat	gtg	ctc	acc	atc	act	ctg	act	cct	531	
Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro		
		160					165					170					
aag	gtc	acg	tgt	gtt	gtg	gta	gac	att	agc	cag	gac	gat	ccc	gag	gtc	579	
Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Gln	Asp	Asp	Pro	Glu	Val		
	175					180					185						
cat	ttc	agc	tgg	ttt	gta	gat	gac	gtg	gaa	gtc	cac	aca	gct	cag	act	627	
His	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr		
190					195					200					205		
cga	cca	cca	gag	gag	cag	ttc	aac	agc	act	ttc	cgc	tca	gtc	agt	gaa	675	
Arg	Pro	Pro	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu		
			210						215					220			
ctc	ccc	atc	ctg	cac	cag	gac	tgg	ctc	aat	ggc	agg	acg	ttc	aga	tgc	723	
Leu	Pro	Ile	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Arg	Thr	Phe	Arg	Cys		
			225					230					235				
aag	gtc	acc	agt	gca	gct	ttc	cca	tcc	ccc	atc	gag	aaa	acc	atc	tcc	771	
Lys	Val	Thr	Ser	Ala	Ala	Phe	Pro	Ser	Pro	Ile	Glu	Lys	Thr	Ile	Ser		
		240					245					250					
aaa	ccc	gaa	ggc	aga	aca	caa	gtt	ccg	cat	gta	tac	acc	atg	tca	cct	819	
Lys	Pro	Glu	Gly	Arg	Thr	Gln	Val	Pro	His	Val	Tyr	Thr	Met	Ser	Pro		
	255					260					265						
acc	aag	gaa	gag	atg	acc	cag	aat	gaa	gtc	agt	atc	acc	tgc	atg	gta	867	
Thr	Lys	Glu	Glu	Met	Thr	Gln	Asn	Glu	Val	Ser	Ile	Thr	Cys	Met	Val		
270					275				280						285		
aaa	ggc	ttc	tat	ccc	cca	gac	att	tat	gtg	gag	tgg	cag	atg	aac	ggg	915	
Lys	Gly	Phe	Tyr	Pro	Pro	Asp	Ile	Tyr	Val	Glu	Trp	Gln	Met	Asn	Gly		
				290					295					300			
cag	cca	cag	gaa	aac	tac	aag	aac	act	cca	cct	acg	atg	gac	aca	gat	963	
Gln	Pro	Gln	Glu	Asn	Tyr	Lys	Asn	Thr	Pro	Pro	Thr	Met	Asp	Thr	Asp		
			305					310					315				
ggg	agt	tac	ttc	ctc	tac	agc	aag	ctc	aat	gtg	aag	aag	gaa	aaa	tgg	1011	
Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Asn	Val	Lys	Lys	Glu	Lys	Trp		
		320					325					330					
cag	cag	gga	aac	acg	ttc	acg	tgt	tct	gtg	ctg	cat	gaa	ggc	ctg	cac	1059	
Gln	Gln	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His		

335	340	345	
aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa			1107
Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln			
350	355	360	365
gat ttt gtg cag tgg ttg atg aat acc tgagaattc			1143
Asp Phe Val Gln Trp Leu Met Asn Thr			
370			
<210>	6		
<211>	825		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29 region		
<220>			
<221>	CDS		
<222>	(13)..(816)		
<223>	DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29 region		
<400>	6		
gaattcattt aa atg aag tcc tgc ggc ctg ttc cct ctc atg gtg ctc ctt			51
Met Lys Ser Cys Gly Leu Phe Pro Leu Met Val Leu Leu			
1	5	10	
gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc gcc gtg			99
Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val			
15	20	25	
ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca			147
Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser			
30	35	40	45
gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc			195
Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu			
50	55	60	
acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc			243
Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser			
65	70	75	
cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa			291
Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu			
80	85	90	
gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act			339
Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr			
95	100	105	
ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat			387
Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn			
110	115	120	125

ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc	435
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro	
130 135 140	
atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat	483
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His	
145 150 155	
gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc	531
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val	
160 165 170	
agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg	579
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val	
175 180 185	
gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca	627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro	
190 195 200 205	
cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat	675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn	
210 215 220	
gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg	723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val	
225 230 235	
ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac	771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His	
240 245 250	
tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc	816
Ser Pro Gly Lys Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr	
255 260 265	
tgagaattc	825
<210> 7	
<211> 1284	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG	
Fc region and glucagons C19-29 region	
<220>	
<221> CDS	
<222> (13)..(1275)	
<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG	
Fc region and glucagons C19-29 region	
<400> 7	
gaattcatitt aa atg gaa atc tgc tgg gga ccc tac agt cac cta atc tct	51

Met	Glu	Ile	Cys	Trp	Gly	Pro	Tyr	Ser	His	Leu	Ile	Ser				
1				5					10							
ctc	ctt	ctc	atc	ctt	ctg	ttt	cat	tca	gag	gca	gcc	tgc	cgc	cct	tct	99
Leu	Leu	Leu	Ile	Leu	Leu	Phe	His	Ser	Glu	Ala	Ala	Cys	Arg	Pro	Ser	
15						20					25					
ggg	aaa	aga	ccc	tgc	aag	atg	caa	gcc	ttc	aga	atc	tggtgat	act	aac		147
Gly	Lys	Arg	Pro	Cys	Lys	Met	Gln	Ala	Phe	Arg	Ile	Trp	Asp	Thr	Asn	
30					35				40						45	
cag	aag	acc	ttt	tac	ctg	aga	aac	aac	cag	ctc	att	gct	ggg	tac	tta	195
Gln	Lys	Thr	Phe	Tyr	Leu	Arg	Asn	Asn	Gln	Leu	Ile	Ala	Gly	Tyr	Leu	
				50					55					60		
caa	gga	cca	aat	atc	aaa	cta	gaa	gaa	aag	ata	gac	atg	gtg	cct	att	243
Gln	Gly	Pro	Asn	Ile	Lys	Leu	Glu	Glu	Lys	Ile	Asp	Met	Val	Pro	Ile	
			65					70					75			
gac	ctt	cat	agt	gtg	ttc	ttg	ggc	atc	cac	ggg	ggc	aag	ctg	tgc	ctg	291
Asp	Leu	His	Ser	Val	Phe	Leu	Gly	Ile	His	Gly	Gly	Lys	Leu	Cys	Leu	
		80					85					90				
tct	tgt	gcc	aag	tct	gga	gat	gat	atc	aag	ctc	cag	ctg	gag	gaa	gtt	339
Ser	Cys	Ala	Lys	Ser	Gly	Asp	Asp	Ile	Lys	Leu	Gln	Leu	Glu	Glu	Val	
95						100					105					
aac	atc	act	gat	ctg	agc	aag	aac	aaa	gaa	gaa	gac	aag	cgc	ttt	acc	387
Asn	Ile	Thr	Asp	Leu	Ser	Lys	Asn	Lys	Glu	Glu	Asp	Lys	Arg	Phe	Thr	
110					115					120					125	
ttc	atc	cgc	tct	gag	aaa	ggc	ccc	acc	acc	agc	ttt	gag	tca	gct	gcc	435
Phe	Ile	Arg	Ser	Glu	Lys	Gly	Pro	Thr	Thr	Ser	Phe	Glu	Ser	Ala	Ala	
				130					135					140		
tgt	cca	gga	tggttc	ctc	tgc	aca	aca	cta	gag	gct	gac	cgt	cct	gtg		483
Cys	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Thr	Leu	Glu	Ala	Asp	Arg	Pro	Val	
			145				150					155				
agc	ctc	acc	aac	aca	ccg	gaa	gag	ccc	ctt	ata	gtc	acg	aag	ttc	tac	531
Ser	Leu	Thr	Asn	Thr	Pro	Glu	Glu	Pro	Leu	Ile	Val	Thr	Lys	Phe	Tyr	
		160					165					170				
ttc	cag	gaa	gac	caa	gcg	gcc	gcc	gtg	ccc	aga	aac	tgt	gga	ggt	gat	579
Phe	Gln	Glu	Asp	Gln	Ala	Ala	Ala	Val	Pro	Arg	Asn	Cys	Gly	Gly	Asp	
	175					180					185					
tgc	aag	cct	tgt	ata	tgt	aca	ggc	tca	gaa	gta	tca	tct	gtc	ttc	atc	627
Cys	Lys	Pro	Cys	Ile	Cys	Thr	Gly	Ser	Glu	Val	Ser	Ser	Val	Phe	Ile	
190					195					200					205	
ttc	ccc	cca	aag	ccc	aaa	gat	gtg	ctc	acc	atc	act	ctg	act	cct	aag	675
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	
				210					215					220		
gtc	acg	tgt	gtt	gtg	gta	gac	att	agc	cag	gac	gat	ccc	gag	gtc	cat	723
Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Gln	Asp	Asp	Pro	Glu	Val	His	

225	230	235	
ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg 240 245 250			771
cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu 255 260 265			819
ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys 270 275 280 285			867
gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys 290 295 300			915
ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr 305 310 315			963
aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys 320 325 330			1011
ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln 335 340 345			1059
cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly 350 355 360 365			1107
agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln 370 375 380			1155
cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn 385 390 395			1203
cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp 400 405 410			1251
ttt gtg cag tgg ttg atg aat acc tgagaattc Phe Val Gln Trp Leu Met Asn Thr 415 420			1284

<210> 8  
 <211> 369  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> DNA insert encoding human IL8 and glucagon C19-29 region

<220>

<221> CDS

<222> (13)..(360)

<223> DNA insert encoding human IL8 and glucagon C19-29 region

<400> 8

```
gaattcattt aa atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc ttc      51
           Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe
                1                5                10
```

```
ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct      99
Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
    15                20                25
```

```
aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac      147
Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
    30                35                40                45
```

```
ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc      195
Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
                50                55                60
```

```
gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt      243
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
    65                70                75
```

```
ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg      291
Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
    80                85                90
```

```
aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt      339
Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe
    95                100                105
```

```
gtg cag tgg ttg atg aat acc tgagaattc      369
Val Gln Trp Leu Met Asn Thr
    110                115
```

<210> 9

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a  
vector pCAGGS-IgG-glul9-29

<400> 9

```
gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg      45
```

<210> 10

<211> 49

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a  
 vector pCAGGS-IgG-glul9-29  
  
 <400> 10  
 tcaaccactg cacaaaatct tgggctttac ccggagagtg ggagagact 49  
  
 <210> 11  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a  
 vector pCAGGS-IgG-glul9-29  
  
 <400> 11  
 gagaattcat ttaaagaga gcggccgccg tgcccagaaa ctgtg 45  
  
 <210> 12  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a  
 vector pCAGGS-IgG-glul9-29  
  
 <400> 12  
 gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc 50  
  
 <210> 13  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a vector  
 pCAGGS-IFN-rR-IgG-glul9-29  
  
 <400> 13  
 gagaattcat ttaaagatt ctgctgggtg tcctgatg 38  
  
 <210> 14  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a vector



pCAGGS-IFN-rR-IgG-glu19-29

<400> 14  
gcagcatcgc ggccgcttct tctctgtcat catggagaaa 40

<210> 15  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used for constructing a vector  
pCAGGS-CTLA4-IgG-glu19-29

<400> 15  
gagaattcat ttaaattggct tgtcttggac tccagagg 38

<210> 16  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used for constructing a vector  
pCAGGS-CTLA4-IgG-glu19-29

<400> 16  
gcagcatcgc ggccgcttct gaatctgggc atggttctgg 40

<210> 17  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used for constructing a vector  
pCAGGS-IL13-IgG-glu19-29

<400> 17  
gagaattcat ttaaattggca ctctgggtga ctgcagtc 38

<210> 18  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used for constructing a vector  
pCAGGS-IL13-IgG-glu19-29

<400> 18  
gcagcatcgc ggccgctgg ccatagcgga aaagttgctt 40

<210> 19  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a vector  
 pCAGGS-IL1RA-IgG-glul9-29  
  
 <400> 19  
 gagaattcat ttaaattggaa atctgctggg gaccctac 38  
  
 <210> 20  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a vector  
 pCAGGS-IL1RA-IgG-glul9-29  
  
 <400> 20  
 gcagcatcgc ggccgcttgg tcttcctgga agtagaactt 40  
  
 <210> 21  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a  
 vector pCAGGS-glul9-29  
  
 <400> 21  
 gagaattcat ttaaattgaga gcggccgccc cgggtaaagc ccaagatttt gtgcagtggg 60  
 tg 62  
  
 <210> 22  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide primer used for constructing a  
 vector pCAGGS-glul9-29  
  
 <400> 22  
 gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc 50  
  
 <210> 23  
 <211> 38  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a  
vector pCAGGS-IL8-glul9-29

<400> 23

gagaattcat ttaaagtact tccaagctgg ccgtggct

38

<210> 24

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a  
vector pCAGGS-IL8-glul9-29

<400> 24

gcagcatcgc ggccgctgaa ttctcagccc tcttcaaaaa

40